

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 23:31:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472658.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472658_1.fastq.gz SRR3472658_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 23:31:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,013,266
Mapped reads	15,879,757 / 99.17%
Unmapped reads	133,509 / 0.83%
Mapped paired reads	15,879,757 / 99.17%
Mapped reads, first in pair	7,974,261 / 49.8%
Mapped reads, second in pair	7,905,496 / 49.37%
Mapped reads, both in pair	15,782,390 / 98.56%
Mapped reads, singletons	97,367 / 0.61%
Secondary alignments	0
Supplementary alignments	91,027 / 0.57%
Read min/max/mean length	30 / 101 / 99.8
Duplicated reads (estimated)	10,986,992 / 68.61%
Duplication rate	48.44%
Clipped reads	998,984 / 6.24%

2.2. ACGT Content

Number/percentage of A's	422,288,436 / 26.97%
Number/percentage of C's	361,985,057 / 23.12%
Number/percentage of T's	425,283,654 / 27.16%
Number/percentage of G's	356,072,035 / 22.74%
Number/percentage of N's	294,887 / 0.02%

GC Percentage	45.86%
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2.3. Coverage

Mean	0.5059
Standard Deviation	24.4634

2.4. Mapping Quality

Mean Mapping Quality	54.71
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2.5. Insert size

Mean	23,308.38
Standard Deviation	1,484,883.68
P25/Median/P75	162 / 221 / 291

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,297,588
Insertions	97,266
Mapped reads with at least one insertion	0.61%
Deletions	83,125
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.52%

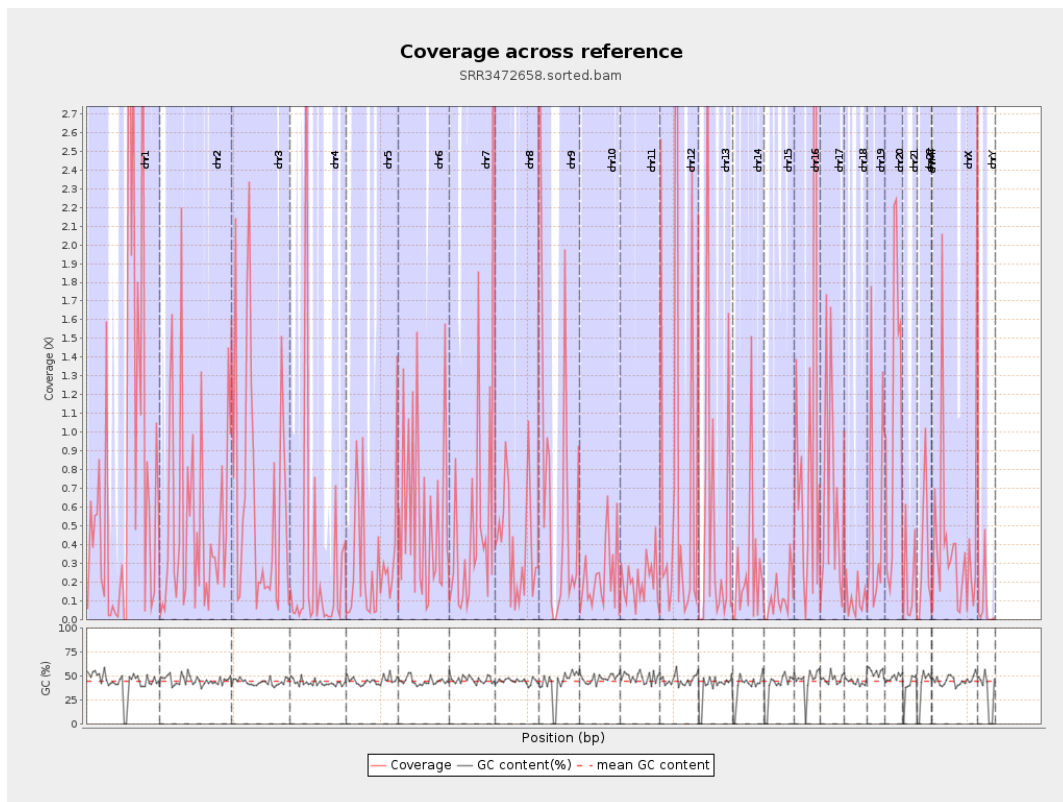
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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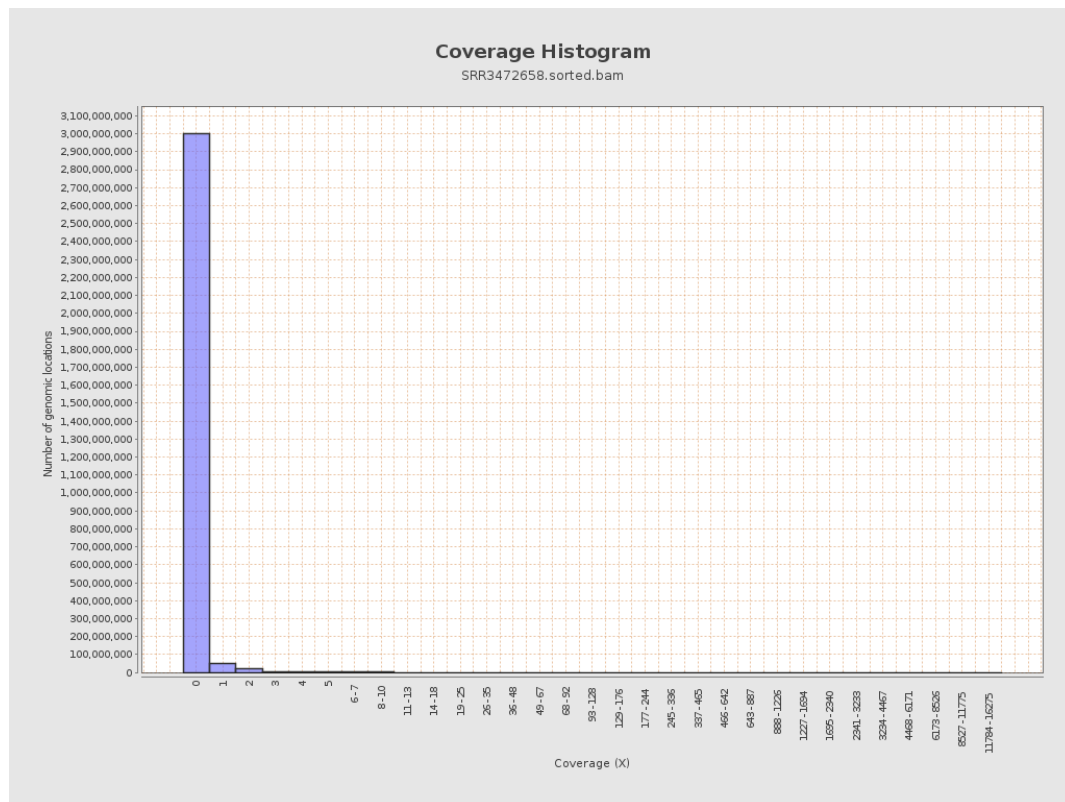
		bases	coverage	deviation
chr1	249250621	199278510	0.7995	38.5698
chr2	243199373	128320037	0.5276	22.4779
chr3	198022430	132499338	0.6691	21.3142
chr4	191154276	52582137	0.2751	22.277
chr5	180915260	55955585	0.3093	13.0806
chr6	171115067	94616948	0.5529	19.8051
chr7	159138663	114871164	0.7218	41.7824
chr8	146364022	59657008	0.4076	12.652
chr9	141213431	101270319	0.7171	29.0943
chr10	135534747	31235808	0.2305	11.1221
chr11	135006516	27706668	0.2052	7.9442
chr12	133851895	112230418	0.8385	37.2592
chr13	115169878	60461384	0.525	27.7747
chr14	107349540	27548860	0.2566	12.3582
chr15	102531392	12069686	0.1177	5.0573
chr16	90354753	94509774	1.046	42.1036
chr17	81195210	54098059	0.6663	20.4636
chr18	78077248	8476166	0.1086	4.5879
chr19	59128983	33963508	0.5744	20.6251
chr20	63025520	70139239	1.1129	33.5153
chr21	48129895	9802173	0.2037	12.3501
chr22	51304566	16886953	0.3292	14.2451
chrMT	16571	5505	0.3322	0.7012
chrX	155270560	63573653	0.4094	11.3274

chrY	59373566	4363904	0.0735	10.6094
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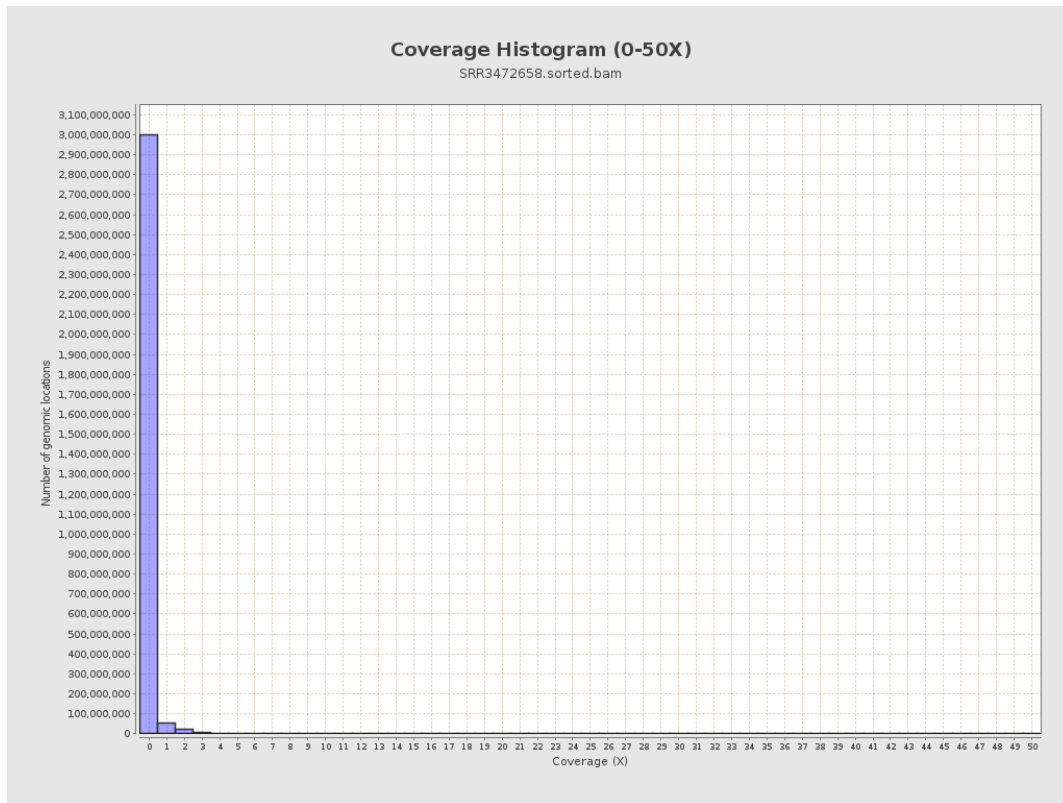
3. Results : Coverage across reference



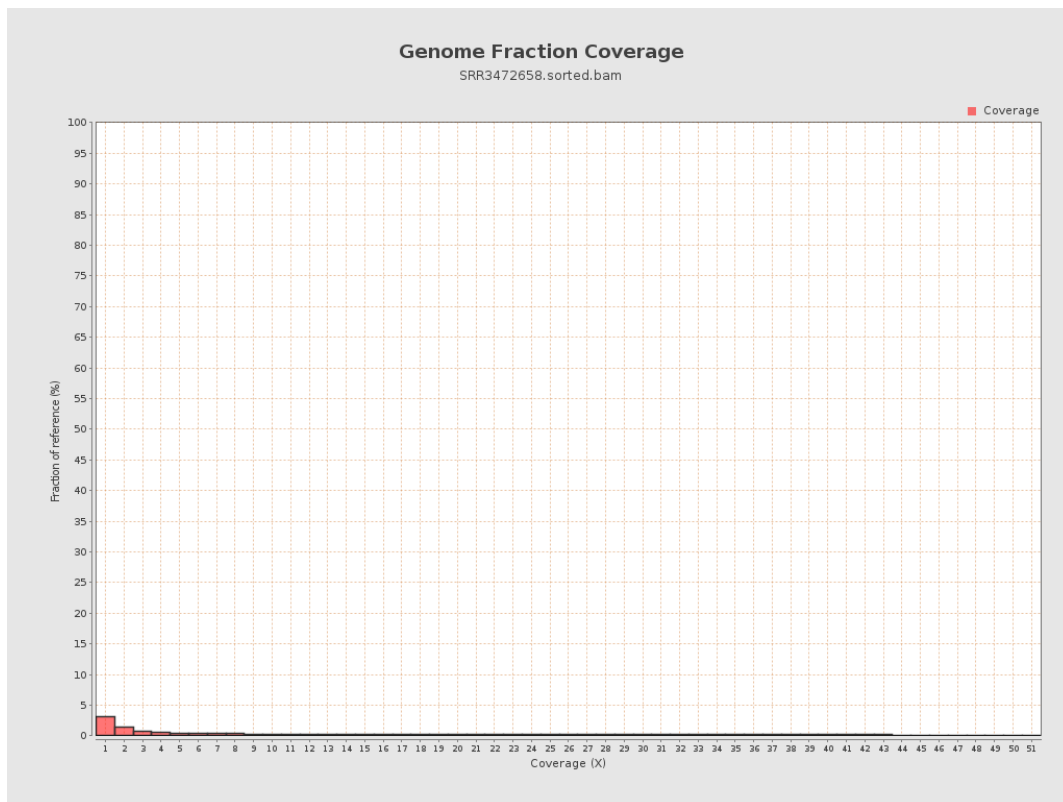
4. Results : Coverage Histogram



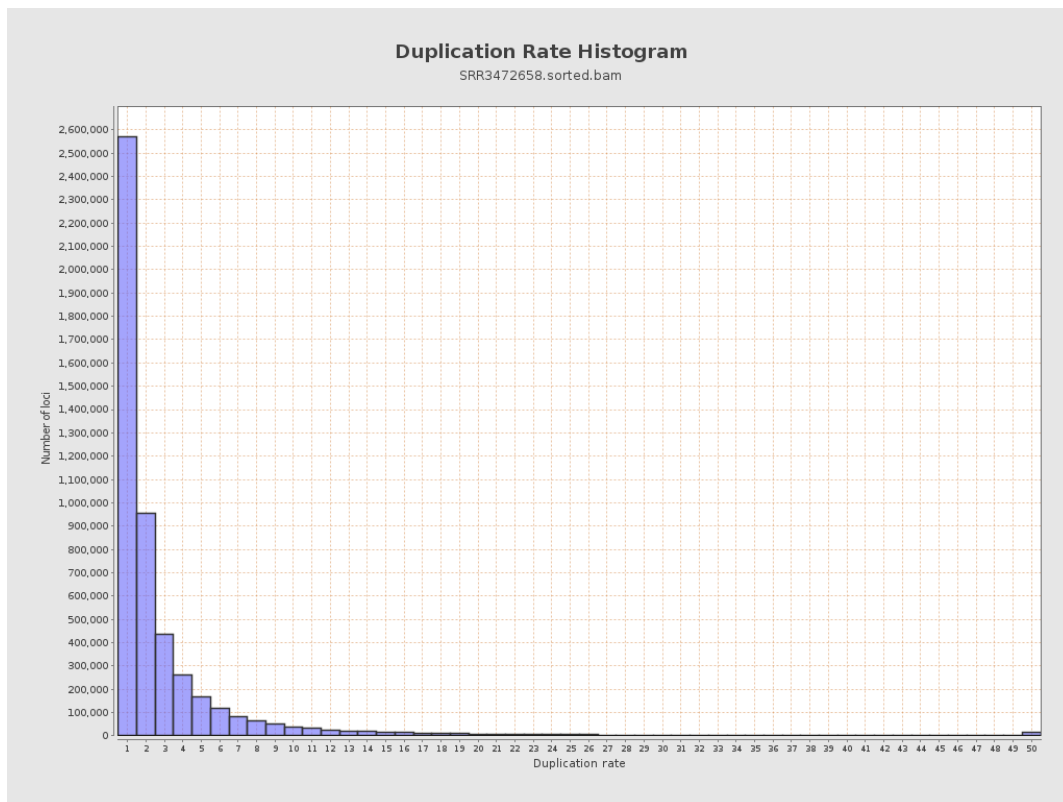
5. Results : Coverage Histogram (0-50X)



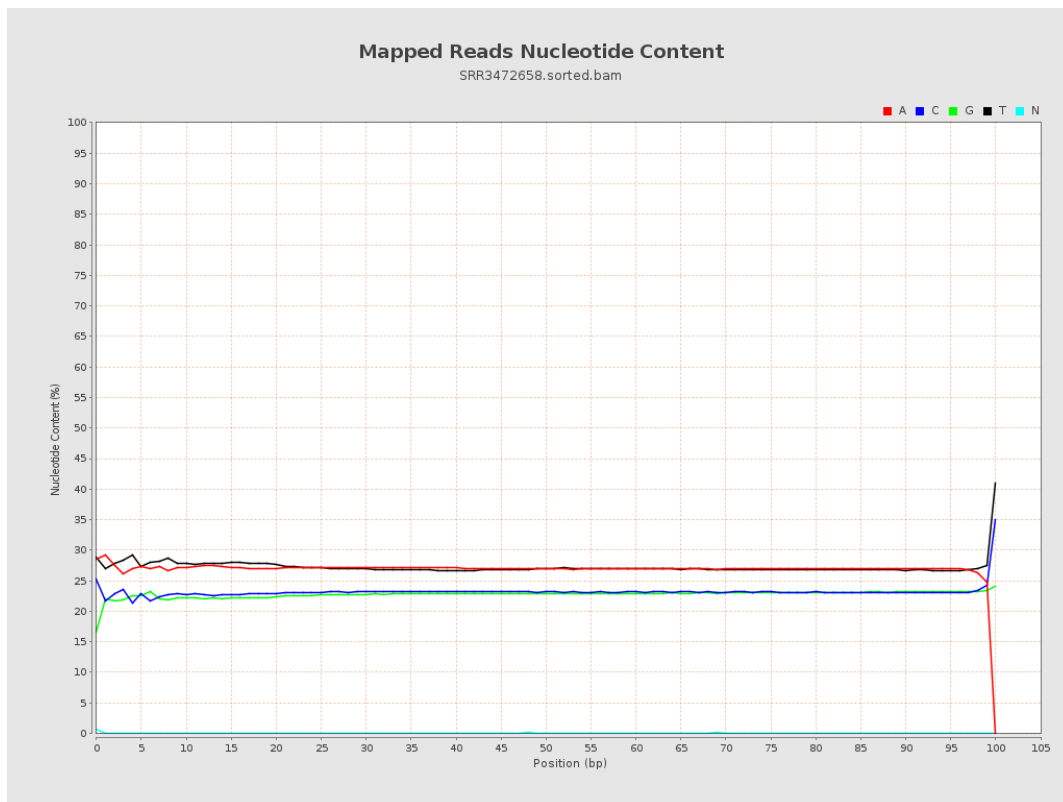
6. Results : Genome Fraction Coverage



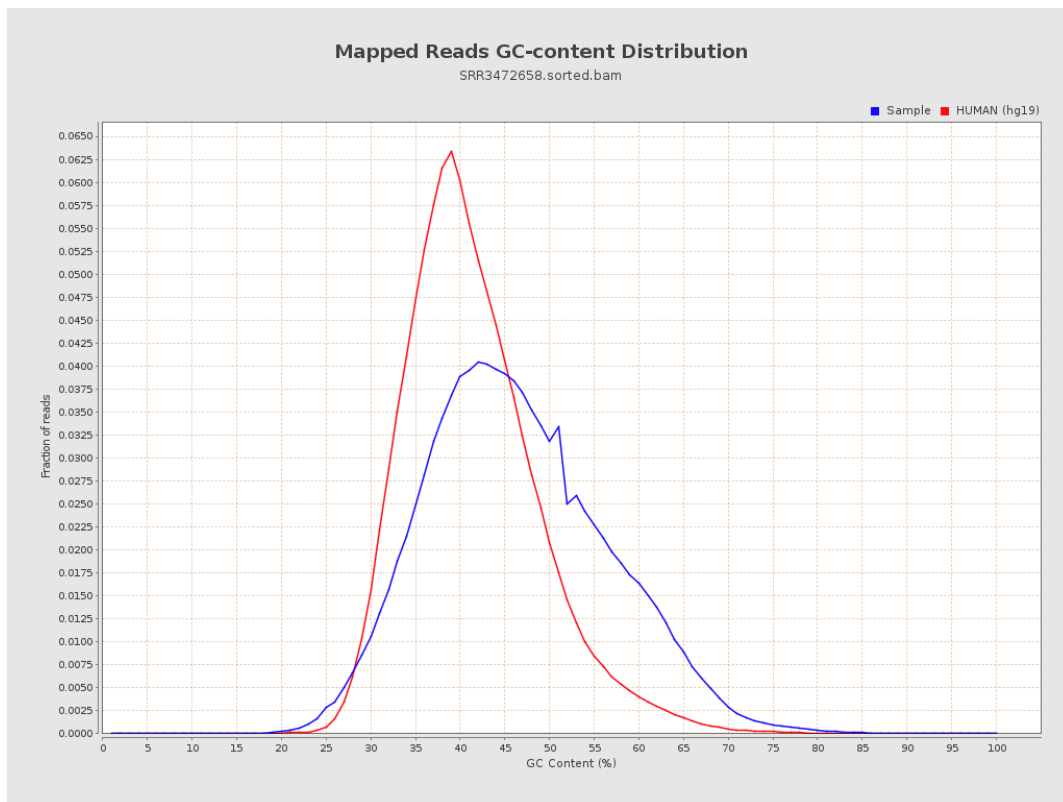
7. Results : Duplication Rate Histogram



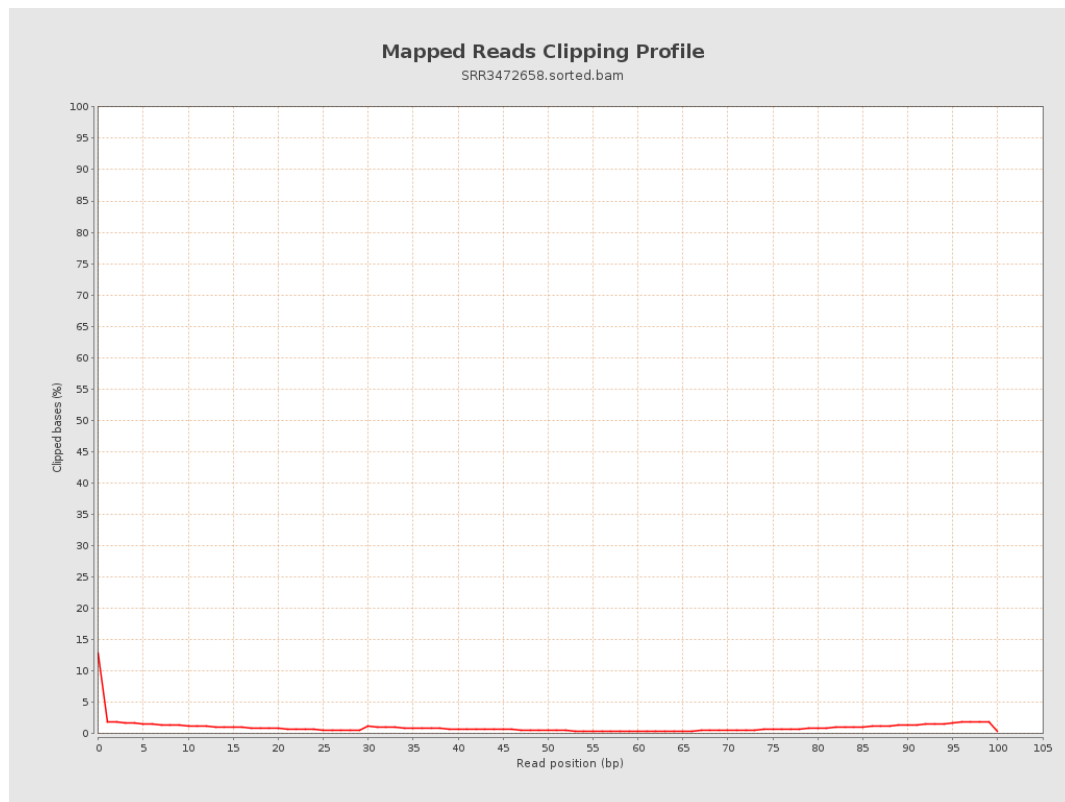
8. Results : Mapped Reads Nucleotide Content



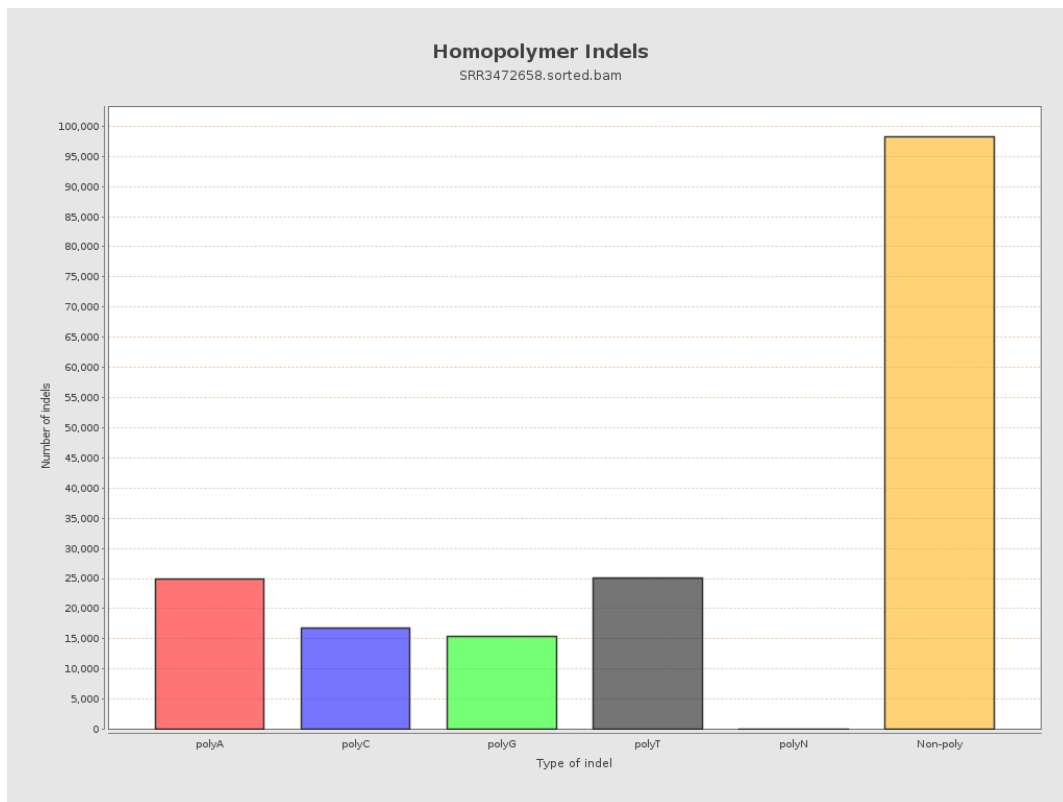
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



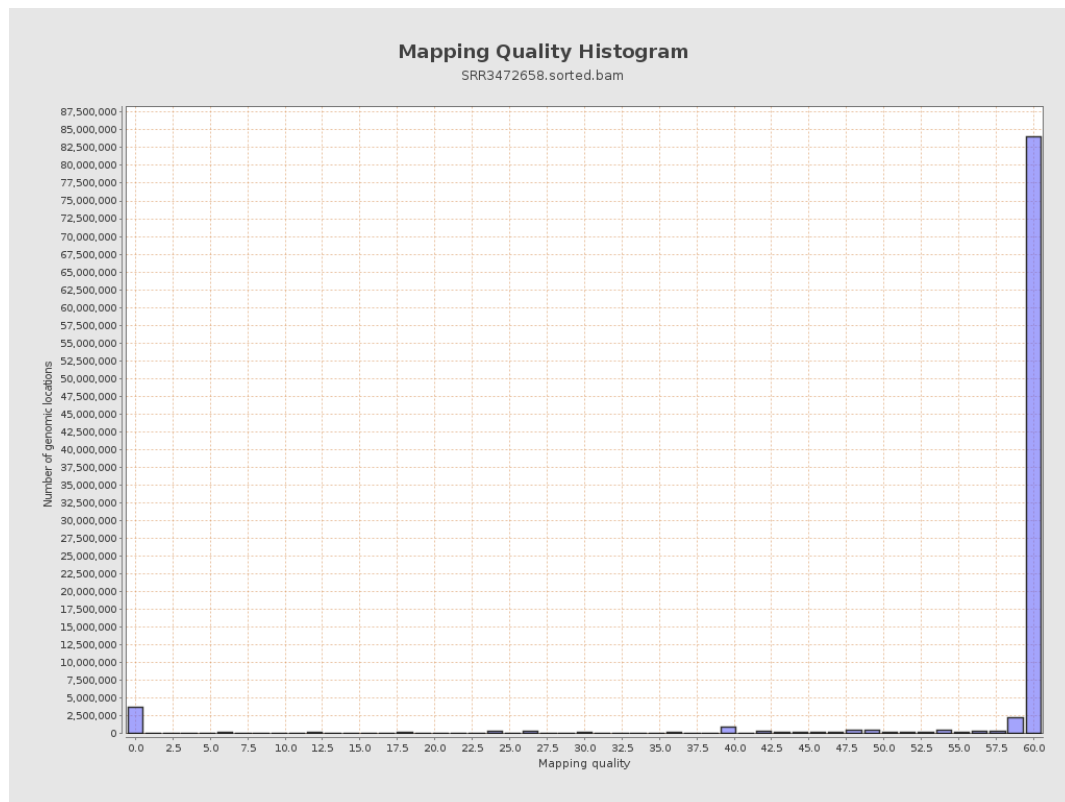
11. Results : Homopolymer Indels



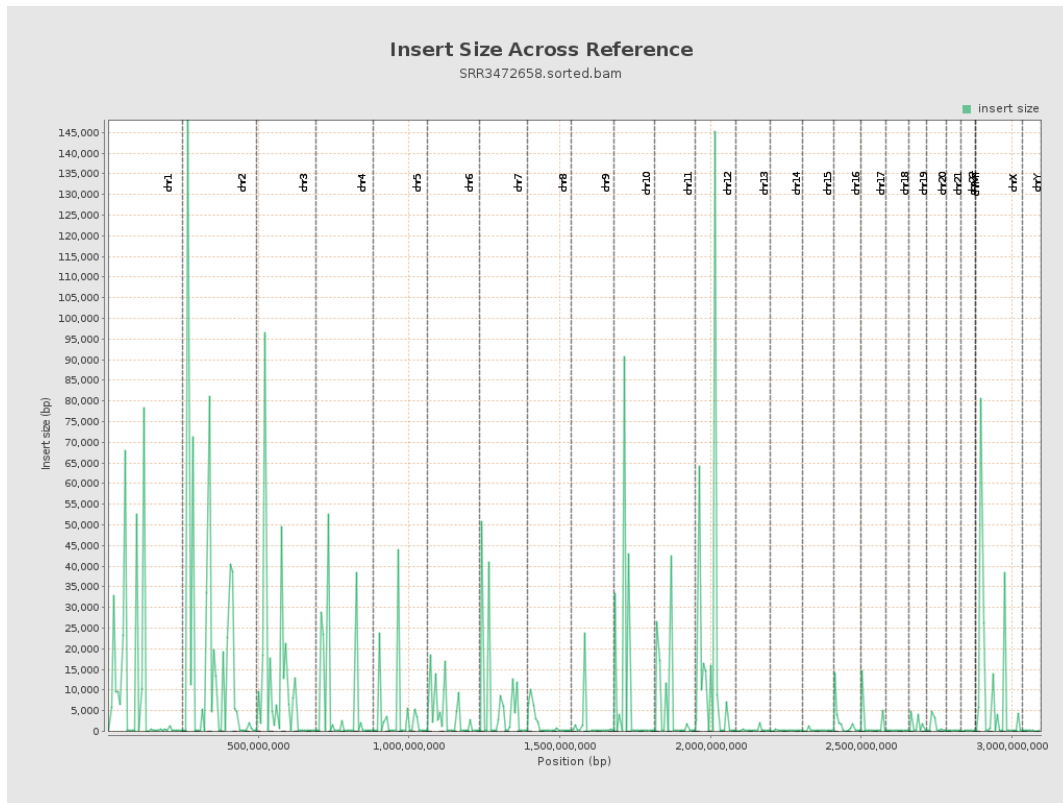
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

